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n Ltd.		me 2144.55 Seconds alignments) Million cell updates/sec	taaggcaacaaaatgattga 484			55026578									predicted by chance to have a score of the result being printed, outal score distribution.	Description	C14748 C14748 Clon AQ990151 R£C00873 D80872 HUM113A12A
(c) 1993 - 2004 Compugen Ltd	using sw model	09:22:37 ; Search time (without al 6739.548 Mi	ggttt	Gapext 1.0	seqs, 14931090276 residues	hits satisfying chosen parameters:	0	0% 1100% 45 summaries					. * * *		esults to the f the t	SUMMARIES ID	C14748 AQ90151 D80872
Copyright (c)	search, us:	15, 2004, (US-09-973-674A-16 484 1 atgcgaattggacacggttt	IDENTITY NUC Gapop 10.0 , Gap		atisfying	2000000000	Match Match first	1	em_esthum:* em_esthum:* em_estin:* em_esten:* em_estpo::* em_estpo::*	htc:* est1:* 5 est2:* 5 htc:*	gb_est4:* gb_est5:* em_estfun:* em_estom:* em_gss_hum:*	em_gss_lnv:* em_gss_pln:* em_gss_vrt:*	em gss mam:* em gss mus:* em gss pro:* em gss rod:* em gss vrl:* ep gss vrl:*	er of equa lysis	Length DB	520 13 699 28 464 14
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302240MO.	397 AG-ND-12. 392 msh2 524. 579 BP132679 39 AV394739 553 EST 5491 190 EST 75957 115 159507 MS	AV62439 AV62439 AV62439 DACS2- 605035D 605063F RTCNT1	Sar83e12 Zea mays CRPT01 CRPT01 CM880021 CRCCR01 CARSTNO	UCKCS02 UCRCS03 NA134 c AV822490 MCR059E sf23d11 EST4751 FGAS027
8 BZ567 8 BZ567 8 AQ991 3 C1506 8 AQ2453 0 BF633 2 BI873 8 BU238	B BH39639 B BZ57709 2 BP13267 AV394739 BQ29655 BQ80049	AV624871 AV624871 AV620733 AV620733 AV620733 AV670587 AIG70587 AIG70587 AIG70587 AIG70587 AIG70587		00007000
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184.4 138.4 13.4 128.4 123 123.4 121.4	120 119 116.6 116 115 115	112.6 112.6 112.0 111.2 111.1 111.1 110.4 109.4	108.6 108.6 108.6 107.2 107 107	105.4 105.4 105.4 105.4 105.4
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ALIGNMENTS

14748/c	
ocus	C14748 520 bp mRNA linear EST 30-SED-1996
EFINITION	A+ mRNA
	clone GEN-086B02 3', mRNA sequence.
CCESSION	C14748
ERSION	C14748.1 GI:1569455
EYWORDS	BST.
DURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi:
	Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
SFERENCE	1 (bases 1 to 520)
AUTHORS	Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M.
	Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya. H.
	Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y.
	Maekawa, H., Shin, S. and Nakamura, Y.
TITLE	Fujiwara et al. (1995)
JOURNAL	Unpublished (1995)
OMMENT	Contact: Tsutomu Fujiwara
	Otsuka GEN Research Institute
	Otsuka Pharmaceutical Co., Ltd
	463-10 kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
	Tel: 0886-65-2888
i	Fax: 0886-37-1035.
ATURES	Location/Qualifiers
source	1520

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ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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                                                                                                                                                                       CGGCAAGCTGTTCCCGGATACCGATCCGGCATTTAAAGGTGCCGATAGCCGCGAGGTGCT 230
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae, Photorhabdus.
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Rfc00873 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00873, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                              231 ACGCGAAGCCTGGCGTCGTATTCAGGCGAAGGGTTATACCCTTGGCAACGTCGATGTCAC
                                                                                                                                                                                                                                                                                                   TATCATCGCTCAGGCACCGAAGATGTTGCCGCACATTCCACAAATGCGCGTGTTTATTGC
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           /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GEN-086690"
/clone="GEN-086690"
/clone_lb="Clontech human aorta polyA+ mRNA (#6572)"
                                                                                                                                         Gaps
                                                                                                                                         4;
                                                                                                          Length 520;
                                                                                                        Score 261.2; DB 13; Length
Pred. No. 4.7e-59;
8; Mismatches 7; Indels
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Contact: ffrench-Constant RH
Department of Baiology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Bmail: bssrfc@bath.ac.uk
organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: M13 Forward
Class: shotgun.
Location/Qualifiers
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93.9%;
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PUBMED
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/organism="Photorhabdus luminescens"

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D80872 464 bp mRNA linear EST 09-FEB-1996 HUM13A12A Human fetal brain (TFujiwara) Homo sapiens cDNA clone GEN-113A12 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                           GGTGGCGTACGCATTCCTTACGAAAAAGGATTGCTGGCGCATTCTGATGGCGACGTGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 TICCCAGATACTGATCCGGCGTTAAAGGGGTGGATAGCCGTAAATTATTGCGCGAAAGCC
                                                                                                                                                                                                                                                       1 ATGCGAATTGGACACGGTTTTGACGTACATGCCTTTGGCGGTGAAGGCCCCAATTATCATT
                                                                                                                                                                                                                       Gaps
                                                                                                                  /note="Genomic DNA from strain W14 was size selected kb) and then cloned into M13 Janus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         420 CGGACGTGGGGAAGGGATTGCCTGTGAAGCGGTGGCGCTACTCATTAAGGCA 471
                                                                /dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14
library"
                                                                                                                                                                                                                       ή;
                                                                                                                                                                                     DB 28; Length 699;
                                                                                                                                                                                                                       Indels
                                                                                                                                                                                     53.8%; Score 260.6; DB 28; 73.3%; Pred. No. 7.6e-59; tive 0; Mismatches 125;
/mol_type="genomic DNA"
                                 xref="taxon:29488"
                                                /clone="PLG00873"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D80872.1 GI:1178749
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                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                           Similarity
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ORGANISM
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COMMENT
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D80872/c
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KEYWORDS
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/clone_lib="WGS-SbicolorF (JM107 adapted methyl filtered)"
/note="Site 1: Xba 1; Site_2: Xba 1; The vector was
digested with Xba1 and one nucleotide was added by fill in
in the recessive 3' end. The genomic DNA was nebulized,
end repaired, adaptor ligated and size fractionated using
sephadex. The resulting fragments were between 0.8 and 3
kb and were cloned into the vector (.x/y reads in M13mp19,
b)g reads in pUC19). The same ligation was transformed in
either JM107 or DH5a."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BZ423610 654 bp DNA linear GSS 10-DEC-2002 id51c09.gl WGS-SbicolorF (DH5a methyl filtered) Sorghum bicolor genomic clone id51c09 5', genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Sorghum.
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                                                                                                                                                                                                                                                                                                                                                                                                 61;
                                                                                                                                                                                                                                                                                                                                   38.5%; Score 186.4; DB 28
llarity 78.5%; Pred. No. 4.9e-39;
Conservative 0; Mismatches 61.
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/mol_type="genomic DNA"
/db_xref="taxon:4558"
/clone="id51c09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 654.
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Plate: id51 row: c column:
Seq primer: -21M13UnivRev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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Sorghum bicolor
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Sorghum bicolor

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatrophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidaee; Andropogoneae; Sorghum.

El (bases 1 to 593)

Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N., Katzenburger, F., King, L., Miller, B., Muller, S., Nascimento, L., Cautavern, T., Palmer, L., McCombie, W.R. and Martienssen, R.A. Genomic shotgun sequences from Sorghum bicolor (methyl-filtered) Unpublished (2002)

Unpublished (2002)

Londact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Fax: 516 367 8884
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hx72g05.g1 WGS-SbicolorF (JM107 adapted methyl filtered) Sorghum
bicolor genomic clone hx72g05 5', genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                             DB 14; Length 464;
                                                                                                                                                                        /dev_stage="fetal"
/clone lib="Human fetal brain (TFujiwara)"
/note="Organ: brain"
                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                          Score 225.4; DB 14
Pred. No. 1.7e-49;
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|mol_type="genomic DNA"
|db_xref="taxon:4558"
|clone="hx72q55"
|lab_host="JM107 or DH5a"
                                                          organism="Homo sapiens"
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Seg primer: -21M13UnivRev
                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
ocation/Qualifiers
                                                                                                                                                  clone="GEN-113A12"
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BZ351818.1 GI:24915450
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/clone_lib="WGS-SbicolorF (DH5a methyl filtered)"
/note="Site_1: Xba I, Site_2: Xba I; The vector was
digested with XbaI and one nucleotide was added by fill in
in the recessive 3' end. The genomic DNA was nebulized,
end repaired, adaptor ligated and size fractionated using
sephadex. The resulting fragments were between 0.8 and 3
kb and were cloned into the vector (.x/y reads in M13mpl9,
b/g reads in pUC19). The same ligation was transformed
into DH5a."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BZ567684 linear GSS 17-DBC-2002 pacs2-164_7159.xl pacs2-164_Peeudomonas aeruginosa genomic clone pacs2-164_7159, genomic survey sequence.
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
/strain="2-164"
/db_xref="taxon:287"
/clone="pacs2-164"
/clone=lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun
library."
                                                                                                                                                                                                                                      Gaps
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Spencer, D. H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings Spencer, D. H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings Burns, J.L., Kaull, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of Seademonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
                                                                                                                                                                                                                                    .
                                                                                                                                                                                                   Length 654;
                                                                                                                                                                                      Score 184.4; DB 28; ......
Pred. No. 1.8e-38;
....r.hes 51; Indels
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University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
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Class: shotgun.
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Contact: ffrench-Constant RH
Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfcobath.ac.uk
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Rfc01133F Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01133F, genomic survey
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Daborn, P. J., Bowen, D. and Blattner, F. R.
Agenomic Sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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Enterobacteriaceae; Photorhabdus.
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0
         Length 1350;
                  28;
Score 138.4; DB 28;
Pred. No. 4.7e-26;
0; Mismatches 177;
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Photorhabdus luminescens
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58.0%;
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us-09-973-674a-16.rst

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al Similarity 95.6%;
151; Conservative
        Local Similarity
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                                                                                                                                              /note="Genomic DNA from strain W14 was size selected (1-2
                                                                                                                                                                                                                                                                                        273
                                                                                                                                                                                                                                                                                                                                                      333
                                                                                                                                                                                                                                                                                                                                                                                90 GGCAATCTGGATATTACGATTATCGCTCAAGCACCCAAAATGCTGCCGCATATTCCACAA 149
                                                                                                                                                                                                                                                                                                                                                                                                                        393
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Latjiwarar, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y., Pujiwara et al. (1995)

Unpublished (1995)
                                                                                                                                                                                                                                                                                                                      68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C15063 310 bp mRNA linear EST 30-SEP-195 C15063 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens CDNA clone GEN-113F02 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
463-10 kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
                                                                                                                                                                                                                                                                                                                30 GATAGCCGTAAATTATTGCGCGAAGCCTATTCACGTATCANAGAAAAGGGTTATCGGATT
                                                                                                                                                                                                                                                                                                                                               274 GGCAACGTCGATGTCACTATCATCGCTCAGGCACCGAAGATGTTGCCGCACATTCCACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                394 ACTACTACGGAAAAACTGGGATTTACCGGACGTGGGAAAGGGATTGCCTGTGAAGCGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                   ATGCGCGTGTTTATTGCCGAAGATCTCGGCTGCCATATGGATGATGTTAACGTGAAAGCC
                                                                                                                                                                                                                                                                                 GATAGCCGCGAGCTGCGCAAGCCTGGCGTCGTATTCAGGCGAAGGGTTATACCCTT
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606".
/clone="GEN-113F02"
/clone_lib="Clontech human aorta polyA+ mRNA (#6572)"
                                                                                             /dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
                                                                                                                                                                                                                                                     .,
                                                                                                                                                                                                                      Length 800;
                                                                                                                                                                                                                 Score 137; DB 28; Length 80
Pred. No. 9.1e-26;
0; Mismatches 76; Indels
                                                                                                                                                             cb) and then cloned into M13 Janus."
               'organism="Photorhabdus luminescens"
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/mol_type="mRNA"
                               /mol_type="genomic DNA"
/strain="W14"
                                                                db_xref="taxon:29488"
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                                                                               'clone="PLG01133F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 454 GCGCTACTCATTAAGGCA 471
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                                                                                                                                                                                                                   28.3%;
70.5%;
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C15063.1 GI:1569770
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                                                                                                                                                                                                              Query Match
Best Local Similarity 70.53
Matches 182; Conservative
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0886-37-1035
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C15063/c
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DB 13; Length 370;

26.4%; Score 128;

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3702-39r Ochrobactrum anthropi BAC Library Ochrobactrum anthropi Genomic clone 3P02-39r, genomic survey sequence.
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Tomkins, J., Miller-Smith, H., Sasinowski, M., Choi, W., Sasinowska, H., Verce, M., Freedman, D., Dean, R. and Wing, R.A.
Physical map and gene survey of the Ochrobactrum anthropi genome using bacterial artificial chromosome contigs
Microb. Comp. Genomics 4 (3), 203-217 (1999)
                                                                           386
                                                                                                                        309
                                                                                                                                                                          446
                                                                                                                                                                                              308 GAAAGCCACTACTACGGAAAA--CTGGATTTACCGGACGT-GGGAARGGATTGCCTGTGA 252
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                                                                                                              368 rccacarargesegrerriarrecegaagareregeerecearargeargreater
                                                                                                                                                              387 GAAAGCCACTACTACGGAAAAACTGGGATTTACCGGACGTGGGGAAGGGATTGCCTGTGA
                                                                   327 ICCACAAAIGCGCGTGTTIATIGCCGAAGAICTCGGCTGCCAIAIGGAIGAIGAIAAACGT
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Ochrobactrum.
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                           Indels
                                                                                                                                                                                                                                                                                         251 AGCGGTGGCGCTACTCATTAAGGCAACAAAATGATTGA 214
                                                                                                                                                                                                                                                             447 AGCGGTGGCGCTACTCATTAAGGCAACAAAATGATTGA 484
Pred. No. 1.7e-23;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clemson University Genomics Institute
Clemson University
100 Uordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 1.
Location/Qualifiers
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AQ242254.1 GI:3688053
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421 246

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Torrez-Jerez, I. (Bases I to 305)

Torrez-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula drought library
Unpublished (2000)
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NF074G12DT1F1099 Drought Medicago truncatula cDNA clone NF074G12DT
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bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                                                                                                                                                                                                                                              305 GCTGCCATATGGATGATGTTAACGTGAAAGCCACTACTACGGAAAAACTGGGATTTACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         422 GACGIGGGGAAGGGATIGCCIGIGAAGCGGTGGCGCIACTACTIAAGGCAACAAAAIGAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245 GACGIGGGGAAGGGATIGCCIGIGAAGCGGIGGCGCIACICATIAAGGCAACAAAATGAI
/dev_stage="Pooled timepoints"
/clone_lib="Drought"
/note="Vector: Lambda Zap; Contains a mixture of entir
plantlets harvested in a series of days-post-watering
timepoints,"
                                                                                                                                                                                                                                                                                                                                       GCTGCCATATGGATGATGTTAACGTGAAAGCCACTACTACGGAAAAACTGGGATTTACCG
                                                                                                                                                                                                                                                                                Gaps
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
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100.0%; Pred. No. 3.4e-22;
ive 0; Mismatches 0;
                                                                                                                                                                                                                         25.4%; Score 123; DB 10;
100.0%; Pred. No. 3.4e-22;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: gdmay@noble.org
Insert Length: 305 Std Error: 0.00
Plate: 074 row: G column: 12
Seq primer: TCACAGGAAACAGCTATGAC.
Location/Qualifiers
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BF634326
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Email: gdmav@noble
                                                                                                                                                                                                                                                                                      Conservative
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BF634326/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    305 bp mRNA linear EST 19-DEC-2000 Medicago truncatula cDNA clone NF072A05DT
                                                          0;
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Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 TGGCGTCGTATTCAGGCGAAGGGTTATACCCTTGGCAACGTCGATGTCACTATCATCGCT 300
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                                                                                                                                                                                                                                     GGTGGCGTACGCATTCCTTACGAAAAAGGATTGCTGGCGCATTCTGATGGCGACGTGGCG 120
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                                                                                                                 1 ATGCGAATTGGACACGCTTTTGACGTACATGCCTTTGGCGGTGAAGGCCCAATTATCATT
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Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, US.
7515 S80 221 7391
Fax: 580 221 7390
Email: gdmay@noble.org
Insert Length: 305 Std Error: 0.00
Plate: 072 row: A column: 05
Seg primer: TCACACAGGAACAGGTATGAC.
                                 Pred. No. 5.4e-23;
0; Mismatches 211;
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/organism="Medicago truncatula"
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/tissue_type="Plantlets"
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/db_xref="taxon:3880"
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BF633873
BF633873.1 GI:11898031
                                    54.5%;
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1 (bases 1 to 305)
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                                                                      253; Conservative
                                          Similarity
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                                          Best Local
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KEYWORDS
SOURCE
ORGANISM
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BF633873/c
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BU238300

DS01_15m07_A DS01_AAFC_ECORC_cold_stressed_Flixweed_seedlings
Descurainia sophia cDNA clone Ds01_15m07, mRNA sequence.
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/db_xref="taxon:89411"
/db_xref="taxon:89411"
/clone="b80115m07"
/tissue_type="laaf, stem"
/dev_stage="1-month seedlings - 1 cm_tall - 8 leaf"
/clone_lib="b801_AAFC_ECORC_cold_stressed_Flixweed_seedlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Descurainia sophia
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
rosids; eurosids II, Brassicales; Brassicaceae; Descurainia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: Bluescript SK+/Xhol-EcoRI, Site 1: Eco RI; Site 2: Xho I; Plants were grown for 1 month at 20oC/16 site 1: Bight/day (average 8 leaves, 1 cm tall, weight 0.02g/plant). Then they were exposed to 2oC, 12 hrs light/day, for 1 week. Library prepared by C. Piche using Stratagene kit."
                                                                                                                                                                                         322 CCAGACACGGACCCCAAGTGGAAGGCGCCCCGCTCGGACATCTTCCTTAAGGAGGCGGTC 381
                                                                                                                                                                                                                                                                                                382 CGGCTGATGGATGAGAGGGTTACGTGCTGGGGAACCTGGACTGCACCATCATCGCGCAG 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                    364 IGCCATATGGATGATGTTAACGTGAAAGCCACTACTACGGAAAAACTGGGATTTACCGGA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 773)
Singh, 7A., Piche, C., Couroux, P., De Moors, A., Harris, L.J.,
Hattori, J. I., Ouellet, T., Robert, L.S., Sprott, D. and Tinker, N.A.
Expressed Sequence Tags from Cold-Stressed Descurainia sophia
                                     CATGCGTTGACCGATGCATTGCTTGGCGCGCGCGCTGGGGGATATCGGCAAGCTGTTC
                                                                                   262 cacaccerdacedacecrarccicescererererecrecaeacarcesceneric
                                                                                                                                                                                                                                             244 CGTCGTATTCAGGCGAAGGGTTATACCCTTGGCAACGTCGATGTCACTATCATCGCTCAG
                                                                                                                                                                                                                                                                                                                                                304 GCACCGAAGATGTTGCCGCACATTCCACAAATGCGCGTGTTTATTGCCGAAGATCTCGGC
                                                                                                                                                                                                                                                                                                                                                                                              442 AAGCCCAAGCTGTCGCCCCACAAGAAGAACATCCGCAACAACCTGAGTGCCATCCTGGGC
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Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 121; DB 13; Length 773; Pred. No. 1.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bmail: singhja@em.agr.ca.
Location/Qualifiers
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Fax: (613) 759-1701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Descurainia sophia
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Unpublished (2001)
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/mol type="mRNA"
/mol type="mRNA"
/strain="Cc-1690 wild type mt+ 21gr"
/db xref='taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Stress condition I,
normalized, Lambda Zap II"
/note="Vector: pBluescript II SK-; Site I: EcoRI; Site 2:
Xho1; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP-N (30 min, lhr, 4hr), TAP-S (30 min, lhr, 4hr), TAP-P (4hr, 12hr, 24hr), NO3 to NH4 (30 min,
lhr, 4hr) and NH4 to NO3 (30min, lhr, 4hr). PolyA mRNA was
purified from each sample, pooled and cDNA synthesized.
The cDNA was directionally cloned into lambda Zap II
(Stratagene) in the EcoRI (5') and XhoRI (3') sites:
pBluescript II SK- plasmide were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."
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305 GCTGCCATAIGGAIGAIGTIAACGIGAAAAGCCACIACTACGGAAAAACTGGGAITTACCG 246
                                                                                   481
                                                                                                                              245 GACGTGGGGAAGGGATTGCCTGTGAAGCGGTGGCGCTACTCATTAAGGCAACAAAATGAT 186
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefebvre, P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants. Project: 963
Contact: Charles Hauser
DCMB Box 91000
                                                                              GACGTGGGGAAGGGATTGCCTGTGAAGCGGTGGCGCTACTCATTAAGGCAACAAAATGAT
                                                                                                                                                                                                                                                                                                                                                                                            963110H07.yl C. reinhardtii CC-1690, Stress condition I, normalized, Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA
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Pred. No. 6.7e-22;
0; Mismatches 212; Indels
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Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
Location/Qualifiers
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msh2_524.y2 msh Pseudomonas aeruginosa genomic clone msh2_5245,
genomic survey sequence.
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas
1 (bases 1 to 811)
Spencer, D.H., Raymond, C.K., Smith, B.E., Sims, E.B., Hastings, M.,
Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of
Psedomonas aeruginosa library
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                                                                                                                                                                                    /organism="Anopheles gambiae"
"mol type="ganomic DNA"
| strain="PEST"
| db_xref="taxon:7165"
| clone="AG-ND-123ELO"
| clone= lib="ND-TAM"
| note="Vector: pECBAC1; Site_1: HindIII"
   University, College Station, Texas 77843-2123,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 120; DB 28;
Pred. No. 3.2e-21;
0; Mismatches 190;
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Contact: Chris K. Raymond
Genome Center
University of Washington
                                                                                                                       Location/Qualifiers
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larity 55.2%;
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This clone is from an A. gambiae BAC library (ND-TAM) provided by
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae BEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M Universty BAC Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 834)
Hong,Y.S., Hogan,J.R., Wang,X., Sarkar,A., Sim,C., Loftus,B.J.,
Ren,C., Huff,E.R., Carlile,J.L., Black,K., Zhang,H.-B.,
Gardner,M.J. and Collins,F.H.
Construction of a BAC library and generation of BAC end
sequence-tagged connectors for genome sequencing of the African
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          recergarrergarecraaarggaaagergerrerrerrerrearcaaagaagerg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGCACCGAAGATGTTGCCGCACATTCCACAAATGCGCGTGTTTATTGCCCGAAGATCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      526 AGAGACCAAAGATAAGTCCTCACAAGGAGAATCCGAYCCAATCTGTCCAAGCTTCTTG
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                                                                       2 TGCGAATTGGACACGGTTTTGACGTACATGCCTTTGGCGGTGAAGGCCCAATTATCATTG
                                                                                                                                 226 Trogaarcesrcaceestrearcracarcracerragaeccaeearaccrrcarcarce
                                                                                                                                                                                              62 GIGGCGIACGCAIICCIIACGAAAAGGAIIGCIGGCGCAIICIGAIGGCGACGIGGCGC
                                                                                                                                                                                                                                     rccargogrigaccgargcarrgccgcgcgcgcgcgcgcgcggararcggcaagcrgr
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
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Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
            Indels
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Anopheles gambiae
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22542063
            1; Mismatches 216;
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                Conservative
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                                                                                                                                                                             /db_xref="raxon:287"
/db_xref="raxon:287"
/done="mah" 2545"
/dlone lib="mah"
/note="Environmental isolate. Whole genomic shotgun
                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                        Length 811;
                                                                                                                                                                                                                                                                                                      Score 119; DB 28; Length 8
Pred. No. 5.9e-21;
0; Mismatches 135; Indels
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 206687244
Email: craymond@u.washington.edu
Class: shotgun.
Location/Qualifiers
1. 911
/organism="Pseudomonas aeruginosa"
/mol type="genomic DNA"
/strain="MSH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 CAGGCACCGAAGATGTTGCCGCACATTCCACAAAT 335
                                                                                                                                                                                                                                                                                                      Query Match 24.6%;
Best Local Similarity 59.7%;
Matches 200; Conservative (
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741 AATCGTTCGAAATTGGTCCGAAATTGAGACCAAT 775

Search completed: June 16, 2004, 06:30:13 Job time : 2152.75 secs